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Sequence#7 : modified

Gene : Erysipelothrix rhusiopathiae spaA gene, partial cds, strain:SE-9

Sequence length: 1748 base pairs

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xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx    48
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
  1             5             10             15

xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx xxx    96
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                20             25             30

xxx xxx xxx xtg att cca cta atc ggt gaa caa gtt gga ttg ctc cca    144
Xaa Xaa Xaa Xaa Ile Pro Leu Ile Gly Glu Gln Val Gly Leu Leu Pro
                35             40             45

gtt tta cct ggg aca ggg ata cat gct cag gaa tac aac aaa atg act    192
Val Leu Pro Gly Thr Gly Ile His Ala Gln Glu Tyr Asn Lys Met Thr
                50             55             60

                                206
gat gct tat att gaa aat ttg gta tct cta att aat caa aaa gtg aag    240
Asp Ala Tyr Ile Glu Asn Leu Val Ser Leu Ile Asn Gln Lys Val Lys
                65             70             75             80

cog ttt ctt ata aat gaa cca aag ggg tac caa agt ttc gaa gca gtg    288
Pro Phe Leu Ile Asn Glu Pro Lys Gly Tyr Gln Ser Phe Glu Ala Val
                85             90             95

aat gaa gag att aac tog att gta agt gaa ctt aaa cat gaa gga atg    336
Asn Glu Glu Ile Asn Ser Ile Val Ser Glu Leu Lys His Glu Gly Met
                100             105             110

agt ctt caa aac att cac cat atg ttt aaa caa agc atc caa aac cta    384
Ser Leu Gln Asn Ile His His Met Phe Lys Gln Ser Ile Gln Asn Leu
                115             120             125

gca act aga atc ggc tac aga agt ttt atg cag gat gct atg tat ctt    432
Ala Thr Arg Ile Gly Tyr Arg Ser Phe Met Gln Asp Ala Met Tyr Leu
                130             135             140

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461
gaa aat ttt gaa aga tta aag att cct gaa ctt gat gaa gca tac gtt 480
Glu Asn Phe Glu Arg Leu Thr Ile Pro Glu Leu Asp Glu Ala Tyr Val
145 150 155 160

gat tta ctc gtg aat tac gag gtg aaa cac cgt att tta gta aaa tat 528
Asp Leu Leu Val Asn Tyr Glu Val Lys His Arg Ile Leu Val Lys Tyr
165 170 175

gaa gat aaa gtt aaa ggt aga got cca tta gaa gca ttt ata gtt cct 576
Glu Asp Lys Val Lys Gly Arg Ala Pro Leu Glu Ala Phe Ile Val Pro
180 185 190

608
cta aga aat aga att cgt agt atg aat gaa att got gca gaa gta aat 624
Leu Arg Asn Arg Ile Arg Ser Met Asn Glu Ile Ala Ala Glu Val Asn
195 200 205

642
tat tta cct gaa gcg cat gag gat ttc tta gtt toa gat toa ago gag 672
Tyr Leu Pro Glu Ala His Glu Asp Phe Leu Val Ser Asp Ser Ser Glu
210 215 220

tat aat gac aaa cta aat aat ato aac ttt got ttg ggt cta ggg gto 720
Tyr Asn Asp Lys Leu Asn Asn Ile Asn Phe Ala Leu Gly Leu Gly Val
225 230 235 240

758
ago gag ttt att gac tat aac cgg ctc gaa aat atg att gaa aaa gaa 768
Ser Glu Phe Ile Asp Tyr Asn Arg Leu Glu Asn Met Met Glu Lys Glu
245 250 255

att cat cca ttg tat ctt gaa ctt tat got atg cgg aga aat cgc caa 816
Ile His Pro Leu Tyr Leu Glu Leu Tyr Ala Met Arg Arg Asn Arg Gln
260 265 270

833
att caa gtt gta aga gat gta tat cca aac ttg gaa cgt gcg aac gcg 864
Ile Gln Val Val Arg Asp Val Tyr Pro Asn Leu Glu Arg Ala Asn Ala
275 280 285

gtt gtt gaa tcc tta aag aca att aaa gat ata aaa caa aga gag aag 912
Val Val Glu Ser Leu Lys Thr Ile Lys Asp Ile Lys Gln Arg Glu Lys
290 295 300

aaa cta cag gaa ctt ctt gaa att tat atc caa aga agt gga gat gtt 960
Lys Leu Gln Glu Leu Leu Glu Ile Tyr Ile Gln Arg Ser Gly Asp Val
305 310 315 320

oga aaa oca gat gta ctc caa oga ttt att gga aaa tat caa tca gta 1008
Arg Lys Pro Asp Val Leu Gln Arg Phe Ile Gly Lys Tyr Gln Ser Val
325 330 335

gtt gat gaa gaa aaa aat aaa ctt caa gat tat tta gaa tca gat att 1056
Val Asp Glu Glu Lys Asn Lys Leu Gln Asp Tyr Leu Glu Ser Asp Ile
340 345 350

ttt gat tca tat agt gtg gat ggc gag aaa ata aga aat aaa gaa att 1104
Phe Asp Ser Tyr Ser Val Asp Gly Glu Lys Ile Arg Asn Lys Glu Ile
355 360 365

aca ctc atc aat aga gat gca tac tta tct atg att tca aga gct caa 1152
Thr Leu Ile Asn Arg Asp Ala Tyr Leu Ser Met Ile Tyr Arg Ala Gln
370 375 380

tgg att tgg gaa att aag aag att ogt goa gat tta gaa tca ott gtc 1200
Ser Ile Ser Glu Ile Lys Thr Ile Arg Ala Asp Leu Glu Ser Leu Val
385 390 395 400

aaa tca ttc caa aat gaa gaa agt gat tct aaa gta gag cct gaa agt 1248
Lys Ser Phe Gln Asn Glu Glu Ser Asp Ser Lys Val Glu Pro Glu Ser
405 410 415

ccc gtt aaa gta gaa aaa oca gtt gat aaa gaa aaa cct aaa gat caa 1296
Pro Val Lys Val Glu Lys Pro Val Asp Lys Glu Lys Pro Lys Asp Gln
420 425 430

aag aag oca gtt gat caa tca aaa ccc gaa tgg aat tca aaa gaa ggg 1344
Lys Lys Pro Val Asp Gln Ser Lys Pro Glu Ser Asn Ser Lys Glu Gly
435 440 445

tgg att aag aaa gat aat aag tgg ttc tat att gag aaa tca ggt gga 1392
Trp Ile Lys Lys Asp Asn Lys Trp Phe Tyr Ile Glu Lys Ser Gly Gly
450 455 460

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atg gca aca gga tgg aag aag gta gga gac aaa tgg tac tac ctc gat      1440
Met Ala Thr Gly Trp Lys Lys Val Gly Asp Lys Trp Tyr Tyr Leu Asp
465              470              475              480

aat acg ggt gct atg gtt acg ggt tgg aag aag gta gca aac aaa tgg      1488
Asn Thr Gly Ala Met Val Thr Gly Trp Lys Lys Val Ala Asn Lys Trp
              485              490              495

tac tac ctt gaa aac tca ggt gcg atg gca aca gga tgg aag aaa gta      1536
Tyr Tyr Leu Glu Asn Ser Gly Ala Met Ala Thr Gly Trp Lys Lys Val
              500              505              510

tca aac aag tgg tac tac ctt gaa aac tca ggt gcg atg gca aca gga      1584
Ser Asn Lys Trp Tyr Tyr Leu Glu Asn Ser Gly Ala Met Ala Thr Gly
              515              520              525
1591
tgg aag aga gta tca aac aag tgg tac tac ctt gaa aat tca ggc gca      1632
Trp Lys Arg Val Ser Asn Lys Trp Tyr Tyr Leu Glu Asn Ser Gly Ala
              530              535              540

atg gct aca gga tgg aaa aag gta gca aac aaa tgg tac tac ctt gaa      1680
Met Ala Thr Gly Trp Lys Lys Val Ala Asn Lys Trp Tyr Tyr Leu Glu
545              550              555              560

aac tca ggt gcg atg gca aca gga tgg aag aaa gta tog aac aag tgg      1728
Asn Ser Gly Ala Met Ala Thr Gly Trp Lys Lys Val Ser Asn Lys Trp
              565              570              575

tac tac ctt gaa aac tca ggc gca atg gca acg ggt tgg aag aaa ata      1776
Tyr Tyr Leu Glu Asn Ser Gly Ala Met Ala Thr Gly Trp Lys Lys Ile
              580              585              590

gca aat aaa tgg tac tac ctt gat aaa tca gga atg atg gtt aca ggt      1824
Ala Asn Lys Trp Tyr Tyr Leu Asp Lys Ser Gly Met Met Val Thr Gly
              595              600              605

tca aaa tot att gat ggt aaa aag tat gca      1854
Ser Lys Ser Ile Asp Gly Lys Lys Tyr Ala
              610              615

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